RAW SEQUENCE LISTING
ERROR REPORT

)TECHNOLOGY
SYSTEMS·
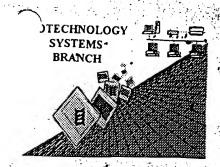BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/831758_

Source: _PCT 09_

Date Processed by STIC: _10/18/01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-42
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker·

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/831758

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

1____Wrapped Nucleics
    Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
    Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length.

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
    "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
    (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
    (NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
    (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10____Invalid <213>
    Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ✓ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
    "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,758   DATE: 10/18/2001
                                             TIME: 09:51:48

Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\10182001\I831758.raw

Does Not Comply
Corrected Diskette Needed

```
         2  <110> APPLICANT: Takeda Chemical Industries, Ltd.
W-->     3  <120> TITLE OF INVENTION: Novel Protein and its DNA
W-->     4  <130> FILE REFERENCE: 2568WOOP
C-->     5  <140> CURRENT APPLICATION NUMBER: US/09/831,758
C-->     5  <141> CURRENT FILING DATE: 2001-08-17
         5  <150> PRIOR APPLICATION NUMBER: JP 10-323759
         6  <151> PRIOR FILING DATE: 1998-11-13
         7  <150> PRIOR APPLICATION NUMBER: JP 11-060030
         8  <151> PRIOR FILING DATE: 1999-03-08
         9  <150> PRIOR APPLICATION NUMBER: JP 11-106812
        10  <151> PRIOR FILING DATE: 1999-04-14
        11  <150> PRIOR APPLICATION NUMBER: JP 11-166672
        12  <151> PRIOR FILING DATE: 1999-06-14
        13  <150> PRIOR APPLICATION NUMBER: JP 11-221640
        14  <151> PRIOR FILING DATE: 1999-08-04
        15  <150> PRIOR APPLICATION NUMBER: JP 11-259818
        16  <151> PRIOR FILING DATE: 1999-09-14
W-->    17  <160> NUMBER OF SEQ ID: 58
W-->    18  <210> SEQ ID NO: 1
        19  <211> LENGTH: 180
        20  <212> TYPE: PRT
        21  <213> ORGANISM: Human
W-->    22  <400> SEQUENCE: 1
        23  Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr
        24   1               5                  10                  15
        25  Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met
        26              20                  25                  30
        27  Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
        28          35                  40                  45
        29  Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
        30       50                  55                  60
        31  Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
        32  65                  70                  75                  80
        33  Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
        34                  85                  90                  95
        35  Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
        36              100                 105                 110
        37  Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
        38          115                 120                 125
        39  Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu
        40       130                 135                 140
        41  Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
        42  145                 150                 155                 160
        43  Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
        44                  165                 170                 175
        45  Lys Gln Ser Arg
        46              180
```

Does Not Comply
Corrected Diskette Needed

Errored: "Artificial Sequence"
in field 213; mandatory
explanation in field 220 is
required.
See page 2 of 9.
See Error Summary Sheet.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

```
         47 <210> SEQ ID NO: 2
         48 <211> LENGTH: 540
         49 <212> TYPE: DNA
         50 <213> ORGANISM: Human
W--> 51 <400> SEQUENCE: 2
C--> 52 atggaaatta tttcatcaaa actattcatt ttattgactt tagccacttc aagcttgtta   60
         53 acatcaaaca tttttgtgc agatgaatta gtgatgtcca atcttcacag caaagaaaat  120
         54 tatgacaaat attctgagcc tagaggatac ccaaaagggg aaagaagcct caattttgag  180
         55 gaattaaaag attggggacc aaaaaatgtt attaagatga gtacacctgc agtcaataaa  240
         56 atgccacact ccttcgccaa cttgccattg agatttggga ggaacgttca agaagaaaga  300
         57 agtgctggag caacagccaa cctgcctctg agatctgga agaaatatgga ggtgagcctc  360
         58 gtgagacgtg ttcctaacct gccccaaagg tttgggagaa caacaacagc caaaagtgtc  420
         59 tgcaggatgc tgagtgattt gtgtcaagga tccatgcatt caccatgtgc caatgactta  480
         60 ttttactcca tgacctgcca gcaccaagaa atccagaatc ccgatcaaaa acagtcaagg  540
         61 <210> SEQ ID NO: 3
         62 <211> LENGTH: 27
         63 <212> TYPE: DNA
         64 <213> ORGANISM: Artificial Sequence
W--> 65 <220> FEATURE:
         66 <223> OTHER INFORMATION:
W--> 67 <400> SEQUENCE: 3
C--> 68 gggctgcaca tagagactta attttag
         69 <210> SEQ ID NO: 4
         70 <211> LENGTH: 27
         71 <212> TYPE: DNA
         72 <213> ORGANISM: Artificial Sequence
W--> 73 <220> FEATURE:
         74 <223> OTHER INFORMATION:
W--> 75 <400> SEQUENCE: 4
C--> 76 ctagaccacc tctatataac tgcccat
         77 <210> SEQ ID NO: 5
         78 <211> LENGTH: 30
         79 <212> TYPE: DNA
         80 <213> ORGANISM: Artificial Sequence
W--> 81 <220> FEATURE:
         82 <223> OTHER INFORMATION:
W--> 83 <400> SEQUENCE: 5
C--> 84 gcacatagag acttaatttt agatttagac
         85 <210> SEQ ID NO: 6
         86 <211> LENGTH: 27
         87 <212> TYPE: DNA
         88 <213> ORGANISM: Artificial Sequence
W--> 89 <220> FEATURE:
         90 <223> OTHER INFORMATION:
W--> 91 <400> SEQUENCE: 6
C--> 92 catgcacttt gactggtttc caggtat
         93 <210> SEQ ID NO: 7
         94 <211> LENGTH: 27
         95 <212> TYPE: DNA
```

Handwritten annotations:

If 213 "Artificial Sequence" Then 223 mandatory explanation

27

If 213 "Artificial Sequence" Then 223 mandatory explanation.

27

Same ...

30

27

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001
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Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\10182001\I831758.raw

```
        96 <213> ORGANISM: Artificial Sequence
W--> 97 <220> FEATURE:
        98 <223> OTHER INFORMATION:
W--> 99 <400> SEQUENCE: 7
C--> 100 cagctttagg gacaggctcc aggtttc                                                27
       101 <210> SEQ ID NO: 8
       102 <211> LENGTH: 196
       103 <212> TYPE: PRT
       104 <213> ORGANISM: Human
W--> 105 <400> SEQUENCE: 8
       106 Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr
       107  1               5                  10                  15
       108 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met
       109             20                  25                  30
       110 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
       111         35                  40                  45
       112 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
       113     50                  55                  60
       114 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
       115 65                  70                  75                  80
       116 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
       117                 85                  90                  95
       118 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
       119             100                 105                 110
       120 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
       121         115                 120                 125
       122 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu
       123     130                 135                 140
       124 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
       125 145                 150                 155                 160
       126 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
       127                 165                 170                 175
       128 Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu
       129             180                 185                 190
       130 Lys Gln Glu Lys
       131             195
       132 <210> SEQ ID NO: 9
       133 <211> LENGTH: 588
       134 <212> TYPE: DNA
       135 <213> ORGANISM: Human
W--> 136 <400> SEQUENCE: 9
C--> 137 atggaaatta tttcatcaaa actattcatt ttattgactt tagccacttc aagcttgtta    60
       138 acatcaaaca ttttttgtgc agatgaatta gtgatgtcca atcttcacag caaagaaaat   120
       139 tatgacaaat attctgagcc tagaggatac ccaaaagggg aaagaagcct caattttgag   180
       140 gaattaaaag attggggacc aaaaaatgtt attaagatga gtacacctgc agtcaataaa   240
       141 atgccacact ccttcgccaa cttgccattg agatttggga ggaacgttca agaagaaaga   300
       142 agtgctggag caacagccaa cctgcctctg agatctggaa gaaatatgga ggtgagcctc   360
       143 gtgagacgtg ttcctaacct gccccaaagg tttgggagaa caacaacagc caaagtgtc    420
       144 tgcaggatgc tgagtgattt gtgtcaagga tccatgcatt caccatgtgc caatgactta   480
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001
TIME: 09:51:48

Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\10182001\I831758.raw

```
        145  ttttactcca tgacctgcca gcaccaagaa atccagaatc ccgatcaaaa acagtcaagg    540
        146  agactgctat tcaagaaaat agatgatgca gaattgaaac aagaaaaa                    588
        147  <210> SEQ ID NO: 10
        148  <211> LENGTH: 27
        149  <212> TYPE: DNA
        150  <213> ORGANISM: Artificial Sequence
W-->    151  <220> FEATURE:
        152  <223> OTHER INFORMATION:
W-->    153  <400> SEQUENCE: 10
C-->    154  gcctagagga gatctaggct gggagga                                             27
        155  <210> SEQ ID NO: 11
        156  <211> LENGTH: 27
        157  <212> TYPE: DNA
        158  <213> ORGANISM: Artificial Sequence
W-->    159  <220> FEATURE:
        160  <223> OTHER INFORMATION:
W-->    161  <400> SEQUENCE: 11
C-->    162  gggaggaaca tggaagaaga aaggagc                                             27
        163  <210> SEQ ID NO: 12
        164  <211> LENGTH: 27
        165  <212> TYPE: DNA
        166  <213> ORGANISM: Artificial Sequence
W-->    167  <220> FEATURE:
        168  <223> OTHER INFORMATION:
W-->    169  <400> SEQUENCE: 12
C-->    170  gatggtgaat gcatggactg ctggagc                                             27
        171  <210> SEQ ID NO: 13
        172  <211> LENGTH: 27
        173  <212> TYPE: DNA
        174  <213> ORGANISM: Artificial Sequence
W-->    175  <220> FEATURE:
        176  <223> OTHER INFORMATION:
W-->    177  <400> SEQUENCE: 13
C-->    178  ttcctcccaa atctcagtgg caggttg                                             27
        179  <210> SEQ ID NO: 14
        180  <211> LENGTH: 196
        181  <212> TYPE: PRT
        182  <213> ORGANISM: Bovine
W-->    183  <400> SEQUENCE: 14
        184  Met Glu Ile Ile Ser Leu Lys Arg Phe Ile Leu Leu Met Leu Ala Thr
        185  1               5                   10                  15
        186  Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Thr Asp Glu Ser Arg Met
        187              20                  25                  30
        188  Pro Asn Leu Tyr Ser Lys Lys Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
        189          35                  40                  45
        190  Gly Asp Leu Gly Trp Glu Lys Glu Arg Ser Leu Thr Phe Glu Glu Val
        191      50                  55                  60
        192  Lys Asp Trp Ala Pro Lys Ile Lys Met Asn Lys Pro Val Val Asn Lys
        193  65                  70                  75                  80
```

```
194 Met Pro Pro Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Met
195                      85                   90                   95
196 Glu Glu Glu Arg Ser Thr Arg Ala Met Ala His Leu Pro Leu Arg Leu
197            100                 105                 110
198 Gly Lys Asn Arg Glu Asp Ser Leu Ser Arg Trp Val Pro Asn Leu Pro
199        115                 120                 125
200 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Ile Thr Lys Thr Leu
201    130                 135                 140
202 Ser Asn Leu Leu Gln Gln Ser Met His Ser Pro Ser Thr Asn Gly Leu
203 145                 150                 155                 160
204 Leu Tyr Ser Met Ala Cys Gln Pro Gln Glu Ile Gln Asn Pro Gly Gln
205                 165                 170                 175
206 Lys Asn Leu Arg Arg Arg Gly Phe Gln Lys Ile Asp Asp Ala Glu Leu
207        180                 185                 190
208 Lys Gln Glu Lys
209        195
211 <210> SEQ ID NO: 15
212 <211> LENGTH: 588
213 <212> TYPE: DNA
214 <213> ORGANISM: Bovine
215 <400> SEQUENCE: 15
216 atggaaatta tttcattaaa acgattcatt ttattgatgt tagccacttc aagcttgtta   60
217 acatcaaaca tcttctgcac agacgaatca aggatgccca atctttacag caaaaagaat  120
218 tatgacaaat attccgagcc tagaggagat ctaggctggg agaaagaaag aagtcttact  180
219 tttgaagaag taaaagattg ggctccaaaa attaagatga ataaacctgt agtcaacaaa  240
220 atgccacctt ctgcagccaa cctgccactg agatttggga ggaacatgga agaagaaagg  300
221 agcactaggg cgatggccca cctgcctctg agactcggaa aaaatagaga ggacagcctc  360
222 tccagatggg tcccaaatct gccccagagg tttggaagaa caacaacagc caaaagcatt  420
223 accaagaccc tgagtaattt gctccagcag tccatgcatt caccatctac caatgggcta  480
224 ctctactcca tggcctgcca gccccaagaa atccagaatc ctggtcaaaa gaacctaagg  540
225 agacggggat ccagaaaat agatgatgca gaattgaaac aagaaaaa              588
227 <210> SEQ ID NO: 16
228 <211> LENGTH: 27
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION:
233 <400> SEQUENCE: 16
234 ccctggggct tcttctgtct tctatgt                                      27
235 <210> SEQ ID NO: 17
236 <211> LENGTH: 26
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION:
241 <400> SEQUENCE: 17
242 agcgattcat tttattgact ttagca                                       26
243 <210> SEQ ID NO: 18
244 <211> LENGTH: 203
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file://C:\Crf3\Outhold\VsrI831758.htm

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/831,758   DATE: 10/18/2001
                                            TIME: 09:51:49

Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\10182001\I831758.raw

```
L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:17 M:283 W: Missing Blank Line separator, <160> field identifier
L:18 M:283 W: Missing Blank Line separator, <210> field identifier
L:22 M:283 W: Missing Blank Line separator, <400> field identifier
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=2
L:65 M:283 W: Missing Blank Line separator, <220> field identifier
L:67 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:112 C: (48) String data converted to lower case,
L:73 M:283 W: Missing Blank Line separator, <220> field identifier
L:75 M:283 W: Missing Blank Line separator, <400> field identifier
L:76 M:112 C: (48) String data converted to lower case,
L:81 M:283 W: Missing Blank Line separator, <220> field identifier
L:83 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:112 C: (48) String data converted to lower case,
L:89 M:283 W: Missing Blank Line separator, <220> field identifier
L:91 M:283 W: Missing Blank Line separator, <400> field identifier
L:92 M:112 C: (48) String data converted to lower case,
L:97 M:283 W: Missing Blank Line separator, <220> field identifier
L:99 M:283 W: Missing Blank Line separator, <400> field identifier
L:100 M:112 C: (48) String data converted to lower case,
L:105 M:283 W: Missing Blank Line separator, <400> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:137 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=9
L:151 M:283 W: Missing Blank Line separator, <220> field identifier
L:153 M:283 W: Missing Blank Line separator, <400> field identifier
L:154 M:112 C: (48) String data converted to lower case,
L:159 M:283 W: Missing Blank Line separator, <220> field identifier
L:161 M:283 W: Missing Blank Line separator, <400> field identifier
L:162 M:112 C: (48) String data converted to lower case,
L:167 M:283 W: Missing Blank Line separator, <220> field identifier
L:169 M:283 W: Missing Blank Line separator, <400> field identifier
L:170 M:112 C: (48) String data converted to lower case,
L:175 M:283 W: Missing Blank Line separator, <220> field identifier
L:177 M:283 W: Missing Blank Line separator, <400> field identifier
L:178 M:112 C: (48) String data converted to lower case,
L:183 M:283 W: Missing Blank Line separator, <400> field identifier
L:215 M:283 W: Missing Blank Line separator, <400> field identifier
L:216 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=15
L:231 M:283 W: Missing Blank Line separator, <220> field identifier
L:233 M:283 W: Missing Blank Line separator, <400> field identifier
L:234 M:112 C: (48) String data converted to lower case,
```
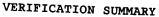
VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/831,758**   DATE: 10/18/2001
                                         TIME: 09:51:49

Input Set : **A:\PTO.MH.txt**
Output Set: **N:\CRF3\10182001\I831758.raw**

```
L:239 M:283 W: Missing Blank Line separator, <220> field identifier
L:241 M:283 W: Missing Blank Line separator, <400> field identifier
L:242 M:112 C: (48) String data converted to lower case,
L:247 M:283 W: Missing Blank Line separator, <400> field identifier
L:278 M:283 W: Missing Blank Line separator, <400> field identifier
L:279 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=19
L:294 M:283 W: Missing Blank Line separator, <220> field identifier
L:296 M:283 W: Missing Blank Line separator, <400> field identifier
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:297 M:112 C: (48) String data converted to lower case,
L:302 M:283 W: Missing Blank Line separator, <220> field identifier
L:304 M:283 W: Missing Blank Line separator, <400> field identifier
L:305 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:305 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:305 M:112 C: (48) String data converted to lower case,
L:310 M:283 W: Missing Blank Line separator, <220> field identifier
L:312 M:283 W: Missing Blank Line separator, <400> field identifier
L:313 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:313 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:313 M:112 C: (48) String data converted to lower case,
L:318 M:283 W: Missing Blank Line separator, <220> field identifier
L:320 M:283 W: Missing Blank Line separator, <400> field identifier
L:321 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:321 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:321 M:112 C: (48) String data converted to lower case,
L:326 M:283 W: Missing Blank Line separator, <220> field identifier
L:328 M:283 W: Missing Blank Line separator, <400> field identifier
L:329 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:329 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:329 M:112 C: (48) String data converted to lower case,
L:334 M:283 W: Missing Blank Line separator, <220> field identifier
L:336 M:283 W: Missing Blank Line separator, <400> field identifier
L:337 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:337 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:337 M:112 C: (48) String data converted to lower case,
L:342 M:283 W: Missing Blank Line separator, <220> field identifier
L:344 M:283 W: Missing Blank Line separator, <400> field identifier
L:345 M:112 C: (48) String data converted to lower case,
L:350 M:283 W: Missing Blank Line separator, <220> field identifier
L:352 M:283 W: Missing Blank Line separator, <400> field identifier
L:353 M:112 C: (48) String data converted to lower case,
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001
TIME: 09:51:49

Input Set : **A:\PTO.MH.txt**
Output Set: **N:\CRF3\10182001\I831758.raw**

```
L:361 M:112 C: (48) String data converted to lower case,
L:369 M:112 C: (48) String data converted to lower case,
L:377 M:112 C: (48) String data converted to lower case,
L:385 M:112 C: (48) String data converted to lower case,
L:393 M:112 C: (48) String data converted to lower case,
L:428 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=34
L:445 M:112 C: (48) String data converted to lower case,
L:453 M:112 C: (48) String data converted to lower case,
L:518 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=38
L:572 M:112 C: (48) String data converted to lower case,
L:578 M:112 C: (48) String data converted to lower case,
L:584 M:112 C: (48) String data converted to lower case,
L:590 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=45
L:600 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=46
L:611 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=47
L:625 M:112 C: (48) String data converted to lower case,
L:633 M:112 C: (48) String data converted to lower case,
L:670 M:112 C: (48) String data converted to lower case,
```